

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

```
Run on:      May 10, 2002, 14:18:50 ; Search time 1794.5 Seconds
              (without alignments)
              90.255 Million cell updates/sec
```

```
Title: US-09-761-116-1
Perfect score: 12
Sequence: 1 gcctctgggag 12
```

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

```
Searched:      13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters:
```

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

```
Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```

1:  estbda:*
2:  em_esthum:*
3:  em_estin:*
4:  em_estum:*
5:  em_estov:*
6:  em_estpl:*
7:  em_estro:*
8:  em_htc:*
9:  gb_estl:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: gb_gss_hum:*
14: gb_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score				Description			
No.	Score	Query	Match	Length	DB	ID		
1	12	100	0	77	10	H55239	H55239	CHR220178 C
C	2	12	100	0	97	AA648867	ns37g08..s	
3	12	100	0	117	9	AM579821	AM579821	RC4-HR027
4	12	100	0	117	9	AM769584	AM769584	bl67g04.x
C	5	12	100	0	121	AI602435	AI602435	ui-R-AGO
C	6	12	100	0	124	BE682645	BE682645	180621 MA
C	7	12	100	0	125	A1712861	A1712861	UI-R-AG1-
8	12	100	0	128	10	BE988071	BE988071	UI-M-GCOP
C	9	12	100	0	129	U25887	U25887	HS025887 Hu
C	10	12	100	0	130	AM530497	AM520497	UI-R-BJOP
C	11	12	100	0	133	AO527525	AO575525	RPCI1-11-3
C	12	100	0	136	12	BF836463	RC3-HR037	
C	13	12	100	0	138	AA955315	AA955315	ui-R-A1-e
C	14	12	100	0	139	BE151130	BE151130	RC4-HR027
C	15	12	100	0	146	AA980863	AA980863	u46e10.r
C	16	12	100	0	154	B87629	B87629	RPCI1-29M1
17	12	100	0	155	12	AZ103219	AZ103219	RPCI1-23-3

C 18	12	100.0	156	10	D77720	D77720 MUSB7D01 mo
C 19	12	100.0	158	9	AA323389	AA323389 EST26257
C 20	12	100.0	163	9	AA719784	AA719784 z38b007.s
C 21	12	100.0	163	12	A2276621	A2276621 RPCT-23-1
C 22	12	100.0	164	10	BG002128	BG002128 QV4-GN025
C 23	12	100.0	168	10	BFE26711	BFE26711 QV4-GN025
C 24	12	100.0	170	9	AV073119	AV073119 AV02070119
C 25	12	100.0	175	9	AA194350	AA194350 z604h07.s
C 26	12	100.0	177	9	AM485310	AM485310 64980 MAR
C 27	12	100.0	180	9	AA339660	AA339660 EST44770
C 28	12	100.0	181	9	AV159589	AV159589 AV159589
C 29	12	100.0	183	10	BF903431	BF903431 IL2-MT017
C 30	12	100.0	183	10	BI034502	BI034502 PM2-NN016
C 31	12	100.0	183	10	BI034708	BI034708 PM2-NN016
C 32	12	100.0	183	12	AO582768	AO582768 RPCT-11-4
C 33	12	100.0	185	10	BF994778	BF994778 QV0-QN021
C 34	12	100.0	186	9	AJ284604	AJ284604 4A3B-AAA-
C 35	12	100.0	186	10	W32815	W32815 zc69e002.r1
C 36	12	100.0	187	9	AI855759	AI855759 sc23g12.y
C 37	12	100.0	187	10	BI289902	BI289902 UI-R-DK0-
C 38	12	100.0	190	9	AM457493	AM457493 UI-M-BH3-
C 39	12	100.0	190	10	N91498	N91498 za91a11.s1
C 40	12	100.0	192	10	BF467452	BF467452 UI-M-CGP0
C 41	12	100.0	194	9	AA543379	AA543379 vJ85a01.s
C 42	12	100.0	194	10	BE936729	BE936729 QV4-OT003
C 43	12	100.0	195	9	AV211454	AV211454 AV211454
C 44	12	100.0	197	12	AZ254882	AZ254882 gss347517
C 45	12	100.0	199	10	BI676845	BI676845 lC56bD10.x

ALIGNMENTS

FEATURES	source
LOCUS	H55239
DEFINITION	77 bp mRNA linear EST 07-DEC-1995
ACCESSION	CH8220178 Chromosome 22 exon Homo sapiens CDNA clone C22_222 5',
VERSION	H55239
KEYWORDS	mRNA sequence.
SOURCE	H55239.1 GI:1108105
ORGANISM	EST.
REFERENCE	human.
AUTHORS	Homo sapiens
TITLE	Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
MEDLINE	1 (bases 1 to 77)
COMMENT	Trofater,J.A., Long,K.R., Murrell,J.R., Stotler,C.J., Gusella,J.F.
	and Buckler,J.J.
	An expression-independent catalog of genes from human chromosome 22
	Genome Res. 5 (3), 214-224 (1995)
	96159527
	Contact: Buckler AJ
	Molecular Neurogenetics Unit
	Massachusetts General Hospital
	Building 149, 13th St., Charlestown MA 02129
	Tel: 6177249616
	Fax: 6177265736
	Email: buckler@helix.mgh.harvard.edu
	Seq primer: T3.
	Location/Qualifiers
	1..77
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone_id="C22_222"
	/clone_lib="Chromosome 22 exon"
	/lab_host="E. coli DH5a"
	/note="Vector: pBluescriptIIKS+; Site_1: Sal I; Site_2:
	Bam HI (destroyed); Exons were isolated from human
	chromosome 22 specific cosmids using a modification of
	the method of exon amplification (Proc. Natl. Acad. Sci.
	USA 88:4005-4009, 1991). Amplified exons were digested
	with Sal I and Bgl II and subsequently cloned into
	pBluescriptIIKS+ at the Sal I and Bam HI sites."

BASE COUNT 15 a 22 c 25 g 15 t
 ORIGIN

Query Match 100.0%; Score 12; DB 10; Length 77;
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gccctcgggag 12
 |||||
 DB 86 GCCTCTGGGAG 75

RESULT 2
 LOCUS AA648867 97 bp mRNA linear EST 29-OCT-1997
 DEFINITION ns37908.s1 NCI-CGAP_GCB1 Homo sapiens CDNA clone IMAGE:1185854 3',
 similar to TR:G984114 G984114 RIBOSOME RECEPTOR.;, mRNA sequence.
 ACCESSION AA648867
 VERSION AA648867.1 GI:2575296
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 97)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncigap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 unknown library type
 Trace considered overall poor quality
 Seq primer: 40m13 fwd. ET from Amerisham
 High quality sequence stop: 1.
 Location/Qualifiers
 1..97
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="1185854"
 /clone_lib="NCI-CGAP_GCB1"
 /issue_type="germlinal center B cell"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand CDNA
 was prepared from human tonsillar cells enriched for
 germinal center B cells by flow sorting (CD20+, IgD-),
 provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
 (NCI) and Dr. Gerald Marti (CBER). CDNA synthesis was
 primed with a Not I - oligo(dT) primer
 [5'-TGTACCACATCGAGTGGAGCGCGCTCATTTTCTTTTCTTTT-3',
]. Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 21 a 29 c 32 g 15 t
 ORIGIN

Query Match 100.0%; Score 12; DB 9; Length 97;
 Best Local Similarity 100.0%; Pred. No. 8.1e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gccctcgggag 12
 |||||
 DB 86 GCCTCTGGGAG 75

RESULT 3
 LOCUS AM579821/C 117 bp mRNA linear EST 16-MAR-2000

DEFINITION RC4-HT0278-080100-012-g04 HT0278 Homo sapiens CDNA, mRNA sequence.
 ACCESSION AM579821
 VERSION AM579821.1 GI:7254870
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 117)
 AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
 TITLE The FAPESP/LICR Human Cancer Genome Project
 JOURNAL Unpublished (1999)
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL.
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=RC4&t2=RC4-HT0278-
 080100-012-g04&t3=2000-01-08&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 8
 High quality sequence stop: 117.
 Location/Qualifiers
 1..117
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="HT0278"
 /dev_strage="Adult"
 /note="Organ: head-neck. Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

BASE COUNT 23 a 38 c 24 g 32 t
 ORIGIN

Query Match 100.0%; Score 12; DB 9; Length 117;
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gccctcgggag 12
 |||||
 DB 20 GCCTCTGGGAG 9

RESULT 4
 LOCUS AM769584 117 bp mRNA linear EST 04-MAY-2000
 DEFINITION h167g04.x1 NCI-CGAP_Kid3 Homo sapiens CDNA clone IMAGE:3006294 3',
 mRNA sequence.
 ACCESSION AM769584
 VERSION AM769584.1 GI:7701616
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 117)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncigap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Chris Moskalko, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@imga.llnl.gov
 Seq primer: -40UP from g1bco
 High quality sequence stop: 107.
 Location/Qualifiers

FEATURES

1. 117
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="3006294"
 /clone_lib="NCI-CGAP_Kid13"
 /tissue_type="2 pooled Wilms' tumors, one primary and one metastatic to brain"
 /lab_host="DH10B"
 /note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: oligo dt. Library constructed by Life Technologies."
 Library constructed by Life Technologies."

BASE COUNT

42 a 24 c 33 g 18 t

ORIGIN

Query Match 100.0%; Score 12; DB 9; Length 117;
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gccctctggggag 12
 |||||

Db 105 gccctctggggag 116

RESULT 5

AI602435 121 bp mRNA linear EST 21-APR-1999
 LOCUS AI602435/c
 DEFINITION UT-R-AG0-wz-g-05-0-UI-s1 UT-R-AG0 Rattus norvegicus cDNA clone

UT-R-AG0-wz-g-05-0-UI 3', mRNA sequence.
 AI602435.1 GI:4611596

ACCESSION

UT-R-AG0-wz-g-05-0-UI 3', mRNA sequence.
 AI602435.1 GI:4611596

KEYWORDS

EST.
 Norway rat.
 Rattus norvegicus

SOURCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murineae;
 Rattus.

REFERENCE

1 (bases 1 to 121)
 Bonaldo,M.F., Lennon,G. and Soares,M.B.

AUTHORS

Normalization and subtraction: two approaches to facilitate gene
 discovery

JOURNAL

Genome Res. 6 (9), 791-806 (1996)

MEDLINE

9704447

COMMENT

Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565

Email: msoares@blue.weeg.uiowa.edu
 The sequence contained an oligo-dt track that was present in the
 oligonucleotide that was used to prime the synthesis of first A
 strand cDNA and therefore this may represent a bonafide poly A
 tail. The sequence tag present in the cDNA between the NotI site
 and the oligo-dt track served to verify it as a clone from the
 non-normalized ventricle at 13 dpc library cDNA library
 preparation: M.B. Soares Lab Clone distribution: clones will be
 available through Research Genetics (www.resgen.com)
 Seg primer: M13 Forward.

FEATURES

Location/Qualifiers
 1. 121
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"

BASE COUNT

25 a 26 c 36 g 34 t

ORIGIN

Query Match 100.0%; Score 12; DB 9; Length 121;
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gccctctggggag 12
 |||||

Db 51 gccctctggggag 40

RESULT 6

BE682645 124 bp mRNA linear EST 25-APR-2001
 LOCUS BE682645
 DEFINITION 180821 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION

BE682645
 BE682645.1 GI:10068717

VERSION

EST.

KEYWORDS

EST.

SOURCE

cow.

ORGANISM

Bos taurus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.

AUTHORS

1 (bases 1 to 124)
 Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
 Casas,E., Wray,J.E., White,J., Cho,J., Fahnenkrug,S.C., Bennett,
 G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitto-McKown,C.G.,
 Pertea,G., Holt,I., Karayancheva,S., Liang,F., Quackenbush,J. and
 Keefe,J.W.

TITLE

Sequence evaluation of four pooled-tissue normalized bovine cDNA
 libraries and construction of a gene index for cattle

JOURNAL

Genome Res. 11 (4), 626-630 (2001)

MEDLINE

21180013

COMMENT

Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390

Email: smith@ma.ars.usda.gov
 Single pass sequencing. Bases called and alt-trimmed with phred
 v0.980904.e. Vector identified by cross-match with the -m1nscore 18
 and -m1nmatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACAT
 BACKWARD: GTTTCACAGTCAGCAGC
 Plate: 75 row: A column: 18
 Seg primer: ATTAGTGTACACTATAG.

FEATURES

Location/Qualifiers
 1. 124
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_lib="MARC 4BOV"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
 Library made from pooled tissue from day 20 and day 40
 embryos."

BASE COUNT 24 a 51 c 33 g 16 t
ORIGIN

Query Match 100.0%; Score 12; DB 10; Length 124;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggcctcgggag 12
|||||
Db 21 GCCTCTGGGAG 32

RESULT 7
AI712861 125 bp mRNA linear EST 08-JUN-1999
LOCUS AI712861
DEFINITION UI-R-AG1-aaf-d-03-0-UI.s2 UI-R-AG1 Rattus norvegicus cDNA clone

ACCESSION AI712861
VERSION AI712861
KEYWORDS AI712861.1 GI:5016661
SOURCE EST.
ORGANISM Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 125)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@iuii.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
M.B. Soares Lab Clone distribution: clones will be available
through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLY-A=yes.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

Location/Qualifiers
1. 125
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-AG1-aaf-d-03-0-UI"
/clone_1b="UI-R-AG1"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pMT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-AG1
library is a normalized library constructed from 13 dpc
rat ventricle. The tag is a string of 6 nucleotides
present between the Not I site and the oligo-dT track.
The library was constructed as described by Bonaldo,
Lennon and Soares, Genome Research 6: 791-806, 1996.
Tissue provided by Jim Lin, Department of Biology,
University of Iowa.
TAG_LIB=UI-R-AG1
TAG_TISSUE=ventricle at 13 dpc
TAG_SEQ=CACGCA"
TAG_SEQ=CGGAG 36 g 35 t

FEATURES

BASE COUNT
ORIGIN

27 a 27 c 36 g 35 t

Query Match 100.0%; Score 12; DB 9; Length 125;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggcctcgggag 12
|||||
Db 52 GCCTCTGGGAG 41

RESULT 8
BE988071 128 bp mRNA linear EST 05-OCT-2000
LOCUS BE988071
DEFINITION UI-M-CG0P-bho-b-02-0-UI.s1 NIH_BMAP_Ret4.S2 Mus musculus cDNA clone

ACCESSION BE988071
VERSION BE988071.1 GI:10664063
KEYWORDS BE988071.1
SOURCE EST.
ORGANISM house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 128)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mst@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA library Preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
clones from RESEARCH GENETICS. It should be noted that Bento Soares
is generating a small number of additional specialized
non-redundant arrays of BMAP cDNAs whose availability will be
considered under appropriate and limited collaborative arrangements
Seq primer: M13 Forward
POLY-A=No.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

Location/Qualifiers
1. 128
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-CG0P-bho-b-02-0-UI"
/clone_1b="NIH_BMAP_Ret4.S2"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pMT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_Ret4.S2 library is a subtracted library,
ultimately derived from mouse retina tissue libraries at
various stages of development. For a detailed description
of the library from which this clone was derived, please
visit our web site at brainest.eng.uiowa.edu.
TAG_SEQ=None found"

FEATURES

source

BASE COUNT 21 a 31 c 35 g 41 t
ORIGIN

Query Match 100.0%; Score 12; DB 10; Length 128;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggcctcgggag 12
|||||
Db 78 GCCTCTGGGAG 89

```

RESULT 9
LOCUS U25887/c 129 bp mRNA linear EST 03-OCT-1995
DEFINITION HSU25887 Human chromosome 12p cDNAs Homo sapiens cDNA clone hsa4,
mRNA sequence.
ACCESSION U25887
VERSION U25887.1 GI:1002430
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 129)
AUTHORS Baens,M., Aerssens,J., Van zand,K., Cassiman,J.J., Van Den Berghe
,H. and Marynen,P.
JOURNAL Isolation and regional assignment of chromosome 12p cDNAs
MEDLINE Genomics 29 (1), 44-52 (1995)
96079090
COMMENT Contact: Peter Marynen
Center for Human Genetics
KULeuven, Herestraat 49, Leuven, B3000, Belgium;
FEATURES
Source
Location/Qualifiers
1..129
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="12p"
/clone="hsa4"
/clone_11b="Human chromosome 12p cDNAs"
BASE COUNT 38 a 26 c 22 g 43 t
ORIGIN
Query Match 100.0%; Score 12; DB 10; Length 129;
Best Local Similarity 100.0%; Pred. NO. 8.7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gccctcggggag 12
|||||
Db 110 gccctcggggag 99

```

M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 95-129, >(GGCA)n#Simple_repeat
Seq primer: M13 forward
POLYA=Yes.

```

FEATURES
Source
Location/Qualifiers
1..130
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-BJ0p-afx-b-09-0-UI"
/clone_11b="UI-R-BJ0p"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pUT73D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; The UI-R-BJ0p
library is a subtracted library derived from the UI-R-A1,
UI-R-A1, UI-R-A1, UI-R-A1, UI-R-A1, UI-R-A1, and
UI-R-A1 libraries. These libraries represent tissues from
rat atrium at 16.5 dpc, ventricle at 16.5 dpc, AV canal
at 16.5 dpc, atrium at 15 dpc, ventricle at 15 dpc, AV
canal at 15 dpc, and ventricle at 13 dpc. The tag is a
string of 5-6 nucleotides present between the Not I site
and the oligo-dT track. The library was constructed as
described by Bonaldo, Lennon and Soares, Genome Research
6: 791-806, 1996.
TAG_LIB=UI-R-BJ0p
TAG_TISSUE=AV canal at 16.5 dpc
TAG_SEO=GNACC"
BASE COUNT 29 a 26 c 41 g 34 t
ORIGIN
Query Match 100.0%; Score 12; DB 9; Length 130;
Best Local Similarity 100.0%; Pred. NO. 8.7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gccctcggggag 12
|||||
Db 51 gccctcggggag 40

```

```

RESULT 11
LOCUS AO527525/c 133 bp DNA linear GSS 18-MAY-1999
DEFINITION RPCI-11-366N14.TV RPCI-11 Homo sapiens genomic clone RPCI-11-366N14
, DNA sequence.
ACCESSION AO527525
VERSION AO527525.1 GI:4839742
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 133)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venier
,J.C.
JOURNAL Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
COMMENT Map Building
Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACpac Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:

```

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: SP6
Class: BAC ends.

FEATURES

source

1.133
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="GDB:7640485"
/db_xref="taxon:9606"
/clone="RPCI-11-366N14"
/clone_1b="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPC11 Human Male BAC library"
BASE COUNT 31 a 43 c 28 g 31 t
ORIGIN

Query Match 100.0%; Score 12; DB 12; Length 133;
Best Local Similarity 100.0%; Pred. No. 8.7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ggcctcgggag 12
|||||
1111111111
Db 92 GCCTCGGGAG 81

RESULT 12
BF836463 136 bp mRNA linear EST 13-JAN-2001
LOCUS RC3-HT0974-171100-012-c02 HT0974 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF836463
ACCESSION BF836463
VERSION BF836463.1 GI:12188356
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 136)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=RC3&cl2=RC3-HT0974-
171100-012-c02&cl3=2000-11-17&cl4=1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence stop: 134.
Location/Qualifiers
1.136
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1b="HT0974"
/dev_stage="Adult"
/note="Organ: head,neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORFESTES PCR (U.S. Letters Patent application

FEATURES

source

No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 35 a 33 c 40 g 28 t
ORIGIN

Query Match 100.0%; Score 12; DB 10; Length 136;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ggcctcgggag 12
|||||
1111111111
Db 81 GCCTCGGGAG 92

RESULT 13
AA955315/c 136 bp mRNA linear EST 04-JUL-1999
LOCUS UI-R-AI-ew-d-02-0-UI.s1 UI-R-AI Rattus norvegicus cDNA clone
DEFINITION UI-R-AI-ew-d-02-0-UI 3', mRNA sequence.
ACCESSION AA955315
VERSION AA955315.1 GI:4237674
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 138)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
On May 7, 1998 this sequence version replaced gi:3118889.
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: mesoares@blue.weeg.iowa.edu

The sequence tag present in the cDNA between the NotI site and the
oligo-dr track served to identify it as a clone from the normalized
adult Heart library. cDNA library Preparation: M. Fatima Bonaldo,
Ph.D. Clone distribution: clones will be available through Research
Genetics. This clone is also available through the I.M.A.G.E.
Consortium at LNL (info@image.lnl.gov). IMAGE ID=1779112 The
following repetitive elements were found in this cDNA sequence:
95-129, >(GGGA)n#Simple_repeat
Seq primer: M13 Forward
POLYA-No.

FEATURES

source

1.138
Location/Qualifiers
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-AI-ew-d-02-0-UI"
/clone_1b="UI-R-AI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7TAD-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-AI
library is a subtracted library derived from the UI-R-A0
library. The UI-R-A0 library consisted of a mixture of
individually tagged normalized libraries constructed from
rat placenta, adult lung, brain, liver, kidney, heart,
spleen, ovary, and muscle. The tag is a string of 3-5
nucleotides present between the Not I site and the
oligo-dr track which allows identification of the library
of origin of a clone within the mixture. The subtracted

library (UT-R-A1) was constructed as follows: PCR amplified cDNA inserts from a pool of approximately 3,840 UT-R-A0 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UT-R-A0 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UT-R-A1 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996).

BASE COUNT 32 a 28 c 44 g 34 t

ORIGIN

Query Match 100.0%; Score 12; DB 9; Length 138;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gccctggggag 12
|||||

Db 51 gccctggggag 40

RESULT 14
BE151130/c 139 bp mRNA linear EST 21-JUN-2000
LOCUS BE151130
DEFINITION RC4-HT0277-160200-013-h05 HT0277 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE151130
VERSION BE151130.1 GI:8613851
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldmann, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunsfeld, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL.
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6&RC4-HT0277-160200-013-h05&tl=2000-02-16&tl=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 139.
Location/Qualifiers
1. 139
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0277"
/dev_stage="Adult"
/note="Organ: head-neck; Vector: puc18; Site:1: Smal; Site:2: Smal; A mini-library was made by cloning products derived from ORESSES PCR (U.S. letters patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of

FEATURES

Source

tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 30 a 45 c 25 g 39 t

ORIGIN

Query Match 100.0%; Score 12; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gccctggggag 12
|||||

Db 43 gccctggggag 32

RESULT 15
AA980863 146 bp mRNA linear EST 27-MAY-1998
LOCUS AA980863
DEFINITION ua46el0.t1 Soares_mammary_gland_NBMKG Mus musculus cDNA clone
IMAGE:1349802 5', mRNA sequence.
ACCESSION AA980863
VERSION AA980863.1 GI:3159399
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Maria, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Maria M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:698594
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 111.
Location/Qualifiers
1. 146
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="1349802"
/clone_lib="Soares_mammary_gland_NBMKG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' TGTTACCAATCTGAGTGAGCGCCGCCGGAATGTTTTTTTTTTTTTTTTTTT T 3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73D vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M. Fatima Bonaldo."

FEATURES

Source

BASE COUNT 32 a 29 c 52 g 33 t

ORIGIN

Query Match 100.0%; Score 12; DB 9; Length 146;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 gcctctggggag 12
|||||
Db 29 GCCTCTGGGAG 40

Search completed: May 10, 2002, 16:46:03
Job time: 8833 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 10, 2002, 14:18:50 ; Search time 1906.21 Seconds
(without alignments)
131.737 Million cell updates/sec

Title: US-09-761-116-1
Perfect score: 12
Sequence: 1 ggcctcggggag 12
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl :
1: gb_ba : *
2: gb_hcg : *
3: gb_in : *
4: gb_om : *
5: gb_ov : *
6: gb_pat : *
7: gb_ph : *
8: gb_pl : *
9: gb_pr : *
10: gb_ro : *
11: gb_sy : *
12: gb_un : *
13: gb_vl : *
14: em_ba : *
15: em_fun : *
16: em_hum : *
17: em_mu : *
18: em_mu : *
19: em_mu : *
20: em_mu : *
21: em_mu : *
22: em_mu : *
23: em_mu : *
24: em_mu : *
25: em_mu : *
26: em_mu : *
27: em_mu : *
28: em_mu : *
29: em_mu : *
30: em_mu : *
31: em_mu : *
32: em_mu : *
33: em_mu : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query Match Length DB ID Description

Result	Query	Match	Length	DB	ID	Description
1	12	100.0	12	6	AR137925	Sequence
2	12	100.0	28	6	AR137965	Sequence
3	12	100.0	28	6	AR137970	Sequence
4	12	100.0	28	6	AR137971	Sequence
5	12	100.0	28	6	AR137972	Sequence
6	12	100.0	130	9	HSU39347	Sequence
7	12	100.0	200	6	AR137927	Sequence
8	12	100.0	208	11	G04524	Sequence
9	12	100.0	234	6	AX244726	Sequence
10	12	100.0	266	11	G65279	Sequence
11	12	100.0	278	9	HSN1243D	Sequence
12	12	100.0	287	9	HMCW05	Sequence
13	12	100.0	292	11	G09804	Sequence
14	12	100.0	321	11	HUW07961A	Sequence
15	12	100.0	330	11	G71854	Sequence
16	12	100.0	343	11	G71018	Sequence
17	12	100.0	370	9	AF366903	Sequence
18	12	100.0	381	6	AX072790	Sequence
19	12	100.0	384	10	MMEB2AK1	Sequence
20	12	100.0	393	10	AF028605	Sequence
21	12	100.0	403	4	AB016736	Sequence
22	12	100.0	403	4	AB016737	Sequence
23	12	100.0	403	4	AB016738	Sequence
24	12	100.0	403	4	AB016739	Sequence
25	12	100.0	403	4	AB016740	Sequence
26	12	100.0	403	4	AB016741	Sequence
27	12	100.0	403	4	AB016742	Sequence
28	12	100.0	403	4	AB016743	Sequence
29	12	100.0	403	4	AB016744	Sequence
30	12	100.0	403	4	AB016745	Sequence
31	12	100.0	417	10	AF028603	Sequence
32	12	100.0	427	11	G55693	Sequence
33	12	100.0	432	10	AF028604	Sequence
34	12	100.0	437	10	MUSX103	Sequence
35	12	100.0	439	4	AB016251	Sequence
36	12	100.0	534	4	DCGP53A	Sequence
37	12	100.0	545	6	AX312180	Sequence
38	12	100.0	591	10	AF300861	Sequence
39	12	100.0	594	10	AF300862	Sequence
40	12	100.0	596	9	HSB323688	Sequence
41	12	100.0	599	9	HSB326032	Sequence
42	12	100.0	599	9	HSB342624	Sequence
43	12	100.0	606	9	HSB338863	Sequence
44	12	100.0	612	9	HSB335324	Sequence
45	12	100.0	612	9	HSB342448	Sequence

ALIGNMENTS

Result	Query	Match	Length	DB	ID	Description
1	12	100.0	12	6	AR137925	Sequence
2	12	100.0	28	6	AR137965	Sequence
3	12	100.0	28	6	AR137970	Sequence
4	12	100.0	28	6	AR137971	Sequence
5	12	100.0	28	6	AR137972	Sequence
6	12	100.0	130	9	HSU39347	Sequence
7	12	100.0	200	6	AR137927	Sequence
8	12	100.0	208	11	G04524	Sequence
9	12	100.0	234	6	AX244726	Sequence
10	12	100.0	266	11	G65279	Sequence
11	12	100.0	278	9	HSN1243D	Sequence
12	12	100.0	287	9	HMCW05	Sequence
13	12	100.0	292	11	G09804	Sequence
14	12	100.0	321	11	HUW07961A	Sequence
15	12	100.0	330	11	G71854	Sequence
16	12	100.0	343	11	G71018	Sequence
17	12	100.0	370	9	AF366903	Sequence
18	12	100.0	381	6	AX072790	Sequence
19	12	100.0	384	10	MMEB2AK1	Sequence
20	12	100.0	393	10	AF028605	Sequence
21	12	100.0	403	4	AB016736	Sequence
22	12	100.0	403	4	AB016737	Sequence
23	12	100.0	403	4	AB016738	Sequence
24	12	100.0	403	4	AB016739	Sequence
25	12	100.0	403	4	AB016740	Sequence
26	12	100.0	403	4	AB016741	Sequence
27	12	100.0	403	4	AB016742	Sequence
28	12	100.0	403	4	AB016743	Sequence
29	12	100.0	403	4	AB016744	Sequence
30	12	100.0	403	4	AB016745	Sequence
31	12	100.0	417	10	AF028603	Sequence
32	12	100.0	427	11	G55693	Sequence
33	12	100.0	432	10	AF028604	Sequence
34	12	100.0	437	10	MUSX103	Sequence
35	12	100.0	439	4	AB016251	Sequence
36	12	100.0	534	4	DCGP53A	Sequence
37	12	100.0	545	6	AX312180	Sequence
38	12	100.0	591	10	AF300861	Sequence
39	12	100.0	594	10	AF300862	Sequence
40	12	100.0	596	9	HSB323688	Sequence
41	12	100.0	599	9	HSB326032	Sequence
42	12	100.0	599	9	HSB342624	Sequence
43	12	100.0	606	9	HSB338863	Sequence
44	12	100.0	612	9	HSB335324	Sequence
45	12	100.0	612	9	HSB342448	Sequence

Query Match

100.0% ; Score 12; DB 6; Length 12;

Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gccctcgggag 12
|||||
Db 1 GCCTCTGGGAG 12

RESULT 2
ARI37965 28 bp DNA linear PAT 16-JUN-2001

LOCUS ARI37965
DEFINITION Sequence 41 from patent US 6197580.
ACCESSION ARI37965
VERSION ARI37965.1 GI:14479474

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 28)
AUTHORS Susulic,V.S. and Duzic,E.

TITLE Transcriptional regulation of the human .beta.3-adrenergic receptor gene
JOURNAL Patent: US 6197580-A 41 06-MAR-2001;

FEATURES
source 1..28
Location/Qualifiers
BASE COUNT 4 a 10 c 8 g 6 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gccctcgggag 12
|||||
Db 6 GCCTCTGGGAG 17

RESULT 3
ARI37970 28 bp DNA linear PAT 16-JUN-2001

LOCUS ARI37970
DEFINITION Sequence 46 from patent US 6197580.
ACCESSION ARI37970
VERSION ARI37970.1 GI:14479479

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 28)
AUTHORS Susulic,V.S. and Duzic,E.

TITLE Transcriptional regulation of the human .beta.3-adrenergic receptor gene
JOURNAL Patent: US 6197580-A 46 06-MAR-2001;

FEATURES
source 1..28
Location/Qualifiers
BASE COUNT 3 a 10 c 8 g 7 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gccctcgggag 12
|||||
Db 6 GCCTCTGGGAG 17

RESULT 4
ARI37971 28 bp DNA linear PAT 16-JUN-2001

LOCUS ARI37971
DEFINITION Sequence 47 from patent US 6197580.
ACCESSION ARI37971
VERSION ARI37971.1 GI:14479480

LOCUS ARI37971

DEFINITION Sequence 47 from patent US 6197580.

ACCESSION ARI37971

VERSION ARI37971.1 GI:14479480

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 28)

AUTHORS Susulic,V.S. and Duzic,E.

TITLE Transcriptional regulation of the human .beta.3-adrenergic receptor gene

JOURNAL Patent: US 6197580-A 47 06-MAR-2001;

FEATURES
source 1..28
Location/Qualifiers
BASE COUNT 6 a 9 c 9 g 4 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gccctcgggag 12
|||||
Db 6 GCCTCTGGGAG 17

RESULT 5
ARI37972 28 bp DNA linear PAT 16-JUN-2001

LOCUS ARI37972
DEFINITION Sequence 48 from patent US 6197580.
ACCESSION ARI37972
VERSION ARI37972.1 GI:14479481

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 28)
AUTHORS Susulic,V.S. and Duzic,E.

TITLE Transcriptional regulation of the human .beta.3-adrenergic receptor gene
JOURNAL Patent: US 6197580-A 48 06-MAR-2001;

FEATURES
source 1..28
Location/Qualifiers
BASE COUNT 5 a 7 c 11 g 5 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gccctcgggag 12
|||||
Db 6 GCCTCTGGGAG 17

RESULT 6
HSU39347 130 bp DNA linear PRI 21-MAR-1997

LOCUS HSU39347
DEFINITION Human MHC class I antigen HLA-C gene (HLA-Cw*0401 allele), Intron
ACCESSION U39347
VERSION U39347.1 GI:1654171

KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 130)
AUTHORS Cered,N., Kong,Y., Lee,S., Maye,P. and Yang,S.Y.

TITLE Nucleotide sequences of MHC class I introns 1, 2, and 3 in humans and intron 2 in nonhuman primates

JOURNAL Tissue Antigens 47 (6), 498-511 (1996)

MEDLINE 96408732

REFERENCE 2 (bases 1 to 130)

AUTHORS Yang, S.Y. and Cereb, N.

TITLE Direct Submission

JOURNAL Submitted (24-OCT-1995) Soo Yang, Immunology Program, Memorial Sloan-Kettering Cancer Center, 1275 York Ave, Box 41, New York, NY 10021, USA

FEATURES Location/Qualifiers

source 1..130
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/map="6p21.3"
/cell_line="WT100BIS B cell line"
1..130
/gene="HLA-C"
1..130
/note="HLA-C*0401 allele"
/number=1

BASE COUNT 19 a 36 c 63 g 12 t

ORIGIN

Query Match 100.0%; Score 12; DB 9; Length 130;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gccctcggggag 12
|||||

Db 27 gccctcggggag 38

RESULT 7

LOCUS ARI37927 200 bp DNA linear PAT 16-JUN-2001

DEFINITION Sequence 3 from patent US 6197580.

ACCESSION ARI37927

VERSION ARI37927.1 GI:14479436.

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 200)
Susulic,V.S. and Duzic,E.
Transcriptional regulation of the human .beta.3-adrenergic receptor gene

JOURNAL Patent: US 6197580-A 3 06-MAR-2001;

FEATURES Location/Qualifiers

source 1..200
/organism="unknown"

BASE COUNT 25 a 70 c 37 g 68 t

ORIGIN

Query Match 100.0%; Score 12; DB 6; Length 200;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gccctcggggag 12
|||||

Db 61 gccctcggggag 72

RESULT 8

LOCUS G04524 208 bp DNA linear STS 19-OCT-1995

DEFINITION human STS WI-4034, sequence tagged site.

ACCESSION G04524

VERSION G04524.1 GI:721482

KEYWORDS STS; STS sequence; primer; sequence tagged site.

SOURCE human Random genome wide STS created from sheared whole human DNA.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS 1 (bases 1 to 208)

TITLE Hudson,T.

JOURNAL Whitehead Institute/MIT Center for Genome Research; Random Genome Wide STS

REFERENCE 2 (bases 1 to 208)

AUTHORS Hudson,T.

TITLE Whitehead Institute/MIT Center for Genome Research; Physically Mapped STS

JOURNAL Unpublished

COMMENT Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: TATGGCAGCTTGAAGAGCG

Primer B: CCCCAAGAGAGCCATCT

STS size: 155

PCR Profile:

Presoak:

Denaturation:

Annealing: 56 degrees C

Polymerization:

PCR Cycles: 35

Thermal Cycler:

Protocol:

Template: 10 ng

Primer: each 5 pm

dNTPs: each 4 mM

Tag Polymerase: 0.025 units/ul

Total Vol: 20 ul

Buffer:

MgCl2: 1.5 mM

KCl: 50 mM

Tris-HCl: 10 mM

pH: 9.3.

FEATURES Location/Qualifiers

source 1..208
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="709.B.4: 802.B.4: 805.F.5: 851.E.2: 964.F.8: 921.A.10: (720,724)_A_(10,12); 304.8 CR from top of Chr15 linkage group"
51..205

STS complement(188..205)

primer_bind 51..70

primer_bind complement(188..205)

BASE COUNT 51 a 43 c 69 g 45 t

ORIGIN

Query Match 100.0%; Score 12; DB 11; Length 208;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gccctcggggag 12
|||||

Db 14 gccctcggggag 25

RESULT 9

LOCUS AX244726 234 bp DNA linear PAT 28-SEP-2001

DEFINITION Sequence 55 from Patent WO0166750.

ACCESSION AX244726 GI:15859605
 VERSION AX244726.1
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 234)
 AUTHORS Vogell, G. and Wood, L.S.
 TITLE G protein-coupled receptors
 JOURNAL Patent: WO 0166750-A 55 13-SEP-2001;
 PHARMACIA & UPJOHN COMPANY (US)
 FEATURES
 source Location/Qualifiers
 1..234
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 56 a 64 c 65 g 49 t
 ORIGIN

Query Match 100.0%; Score 12; DB 6; Length 234;
 Best Local Similarity 100.0%; Pred. NO. 4.2e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gccctctggggag 12
 |||||||||
 Db 100 GCCTCTGGGAG 111

RESULT 10
 G65279 266 bp DNA linear STS 14-JUL-2000
 LOCUS FBNI-64new Random genomic STS Homo sapiens STS genomic, sequence
 DEFINITION tagged site.
 G65279
 ACCESSION G65279.1 GI:9211115
 VERSION STS.
 KEYWORDS human.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 266)
 AUTHORS Oefner, P.J.
 TITLE Human random genomic STS survey, unpublished data
 JOURNAL Unpublished
 COMMENT
 Contact: Peter Oefner
 Stanford Genome Center
 Stanford University
 855 California Ave., Palo Alto, CA 94304, USA
 Tel: 6508121926
 Fax: 6508121975
 Email: Oefner@genome.stanford.edu
 Primer A: CCTACCTTGTCTCCCACTTAA
 Primer B: ACAGAGACATCAGGAGAACTAAC
 STS size: 266
 PCR Profile:
 Initial denaturing step of 95 degrees C for 10 min to activate
 AmpliTaq Gold (1
 min for AmpliTaq);
 14 cycles of touchdown: 94 degrees C for 20 sec, annealing for 1
 min at 63
 degrees C to
 56 degrees C using decrements of 0.5 degrees C, extension at 72
 degrees C for 1
 min;
 20 cycles at 94 degrees C for 20s, 56 degrees C for 45 sec, 72
 degrees C for 1
 min.
 Protocol:
 Template: 50 ng
 Primer: each 0.2 uM
 Taq Polymerase: 0.02 units/ul

Total Vol: 50 ul

Buffer: 2.5 mM
 MgCl2: 50 mM
 KCl: 10 mM
 Tris-HCl: 8.3
 pH:
 DMSO: 0 %

FEATURES
 source Location/Qualifiers
 1..266
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /sex="Male and Female"
 /clone_lib="Random genomic STS"
 1..266
 primer_bind 1..23
 primer_bind complement(242..266)
 BASE COUNT 69 a 68 c 65 g 64 t
 ORIGIN

Query Match 100.0%; Score 12; DB 11; Length 266;
 Best Local Similarity 100.0%; Pred. NO. 4.1e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gccctctggggag 12
 |||||||||
 Db 145 GCCTCTGGGAG 134

RESULT 11
 HSNL1243D 278 bp DNA linear PRI 01-JUL-1996
 LOCUS HSNL1243D
 DEFINITION H.sapiens genomic DNA (chromosome 3; clone NLI243D).
 X87489
 ACCESSION X87489.1 GI:1418839
 VERSION
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 278)
 AUTHORS Zabarovsky, E.R.
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 278)
 AUTHORS Zabarovsky, E.R.
 TITLE Direct Submission
 JOURNAL Submitted (03-MAY-1995) Zabarovsky E.R., Microbiology and
 Tumorbiology Center, Karolinska Institute, P.O. Box 280, Stockholm,
 S-171 77, SWEDEN
 FEATURES
 source Location/Qualifiers
 1..278
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="3 (human)"
 /cell_line="mouse/human microcell hybrid line MHC 903.1"
 /clone_lib="NLI243D"
 /note="genomic DNA surrounding NotI sites"
 BASE COUNT 44 a 95 c 77 g 62 t
 ORIGIN

Query Match 100.0%; Score 12; DB 9; Length 278;
 Best Local Similarity 100.0%; Pred. NO. 4.1e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gccctctggggag 12
 |||||||||
 Db 240 GCCTCTGGGAG 251

RESULT 12

HUMCW05/c
 LOCUS HUMCW05 287 bp DNA linear PRI 14-APR-2000
 DEFINITION Human DNA for HLA-Cw*0702, partial cds.
 ACCESSION D64153
 VERSION D64153.1 GI:1339908
 KEYWORDS HLA-Cw*0702; MHC class I.
 SOURCE Homo sapiens (Isolate:TM) peripheral blood lymphocyte DNA, clone:U-1.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 287)
 AUTHORS Wang, H., Tokunaga, K., Ishikawa, Y., Asahina, A., Kuwata, S., Akaza, T., Tadokoro, K., Shibata, Y., Takiguchi, M. and Uji, T.
 TITLE Identification and DNA typing of two Cw7 alleles (Cw*0702 and Cw*0704) in Japanese, with the corrected sequence of Cw*0702
 JOURNAL Hum. Immunol. 45 (1), 52-58 (1996)
 MEDLINE 96232973
 REFERENCE 2 (bases 1 to 287)
 AUTHORS Wang, H.
 JOURNAL Unpublished (1996)
 REFERENCE 3 (bases 1 to 287)
 AUTHORS Wang, H.
 TITLE Direct Submission
 JOURNAL Submitted (16-SEP-1995) Huiru Wang, Japanese Red Cross Central Blood Center, Department of Research, 4-1-31 Hiroo, Shibuya-ku, Tokyo 150, Japan (Tel:03-3485-6009, Fax:03-3406-7892)
 FEATURES
 source
 1..287
 /organism="Homo sapiens"
 /isolate="TM"
 /db_xref="taxon:9606"
 /chromosome="6"
 /map="6p21.3"
 /clone="U-1"
 /cell_type="lymphocyte"
 /tissue_type="peripheral blood"
 1..157
 /number=1
 85..>157
 /codon_start=1
 /product="HLA-Cw*0702"
 /protein_id="BAI1022.1"
 /db_xref="GI:1561555"
 /translation="MKVMAFRLLILSLALLETWA"
 158..287
 /number=1
 101 c 103 g 38 t
 BASE COUNT 45 a 101 c 103 g 38 t
 ORIGIN
 Intron
 Query Match 100.0%; Score 12; DB 9; Length 287;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 gacctcggagg 12
 |||||||||
 Db 80 GCCTCTGGGAG 69.
 RESULT 13
 LOCUS G09804 292 bp DNA linear STS 15-AUG-1995
 DEFINITION Human STS CHLC.GCT13C07.PI6417 clone GCT13C07, sequence tagged site.
 ACCESSION G09804
 VERSION G09804.1 GI:941653
 KEYWORDS STS; STS sequence; primer; sequence tagged site.
 SOURCE human vector-pUCP1 host-E.coli dutung? (DH10B) Marker Selected genomic DNA prepared from XY individual of French nationality.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 292)
 AUTHORS Murray, J., Sheffield, V., Weber, J.L., Duyk, G. and Buettow, K.H.
 TITLE Cooperative Human Linkage Center
 JOURNAL Unpublished
 COMMENT Synonyms: GCT13C07, CHLC.GCT13C07.T16344
 Contact: Dr. Jeffrey C. Murray
 UofI
 The University of Iowa
 Department of Pediatrics, Iowa City, IA 52242, USA
 Tel: (319) 356-3508
 Fax: (319) 356-3347
 Email: jeff-murray@iowa.edu
 Primer A: TTCGACCTTACCATGTTGATCC
 Primer B: GTTCACCTGACACAGTTCCC
 STS size: 122
 PCR Profile:
 denature: 30 seconds at 94 degrees C
 annealing: 75 seconds at 55 degrees C
 extension: 15 seconds at 72 degrees C
 PCR cycles: 27
 extension: 6 minutes at 72 degrees C
 Protocol:
 Template: 30ng genomic DNA
 Primer: each 1.5 pmole
 dNTPs: each 200 uM
 Taq Polymerase: 0.3 units
 Total Vol: 10 uL
 Buffer:
 MgCl2: 1.5mM
 KCl: 50mM
 Tris: 10mM
 pH: 8.3
 Location/Qualifiers
 1..292
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 62..183
 complement(164..183)
 86 a 60 c 58 g 86 t 2 others
 BASE COUNT 86 a 60 c 58 g 86 t 2 others
 ORIGIN
 STS
 primer_bind
 primer_bind
 Query Match 100.0%; Score 12; DB 11; Length 292;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 gacctcggagg 12
 |||||||||
 Db 219 GCCTCTGGGAG 230
 RESULT 14
 LOCUS HUMUT7961A/c 321 bp DNA linear STS 29-DEC-1994
 DEFINITION Human STS UT7961, 5' primer bind, sequence tagged site.
 ACCESSION L30159
 VERSION L30159.1 GI:605335
 KEYWORDS STS; PCR primer; STS sequence; microsatellite DNA; microsatellite marker; sequence tagged site; tetranucleotide repeat.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 321)
 AUTHORS Gerken, S.C., Matsunami, N., Plaetke, R., Albertsen, H., Ballard, L., Wells, R., Lawrence, E., Moore, M., Holik, P.R., Carlson, M., Zhao, X., Robertson, M., Bradley, P., Elsner, T., Tingey, A., Lalouel, J.-M. and White, R.
 TITLE Genetic and physical mapping of simple sequence repeat containing

JOURNAL
COMMENT

Sequence tagged sites from the human genome
Unpublished (1994)

Submitted by: Utah Center for Human Genome Research University of
Utah, Dept. of Human Genetics

2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112

e-mail: stgcorona.med.utah.edu

Primer A: TTGGACTCCCGACAGCGT

Primer B: TTGGCTGGCGCTGTAGTTT

End to Label: Primer A

PCR Profile:

Initial Denaturation: 94C 300sec

Cycles Denaturation: 94C 30 sec

34 C 10 sec. 72 C 20 sec. 94 C 10 sec.

56 C 10 sec. 72 C 20 sec. Mg++: 1.00 mM

gel: Acrylamide 7%, Formamide 32%, Urea 34%

Alleles: 1.

Location/Qualifiers

1..321

/organism="Homo sapiens"

/db_xref="taxon:9606"

197..215

/evidence=experimental

64 a 102 c 97 g 53 t 5 others

BASE COUNT

ORIGIN

prfmer_bind

Query Match

Best Local Similarity 100.0%; Score 12; DB 11; Length 321;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 1 gcctctgaggag 12

|||||

DB 213 GCCTCTGGGAG 202

RESULT 15

G71854

LOCUS A09122834FW017 maize leaf DNA 330 bp DNA 11 linear STS 08-JUN-2001

DEFINITION site.

ACCESSION G71854

VERSION G71854.1 GI:1433539

KEYWORDS STS.

SOURCE Zea mays.

ORGANISM Zea mays.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 330)

Yang, Y.J., Guo, L., Ashlock, D.A., Wen, T.J. and Schnable, P.S.

3' UTR sequences of maize genes

Unpublished

Contact: Schnable, P.S.

Schnable Laboratory

Iowa State University

G405 Agronomy Hall, Ames, IA 50011, USA

Tel: 515-294-0975

Fax: 515-294-2299

Email: schnable@iastate.edu

Primer A: CCTATCTATGGCTTCACG

Primer B: GGAGAGGCTGATCATCG

PCR Profile:

Denaturation: 94 degrees C for 30 seconds

Annealing: 60 degrees C for 45 seconds

Polymerization: 72 degrees C for 90 seconds

PCR cycles: 31

Thermal cycler: Perkin Elmer TC

Protocol:

Template: 10-20 ng

Primer: each 0.5 uM

dNTPs: each 200 uM

Tag Polymerase: 0.05 units/ul
Total vol: 20 ul

Buffer:

MgCl2: 2 mM

KCl: 50 mM

Tris-HCl: 20 mM

pH: 8.4

Location/Qualifiers

1..330

/organism="Zea mays"

/strain="DE811"

/db_xref="taxon:4577"

/clone.lib="maize leaf DNA"

/note="PCR products amplified from genomic DNA"

<1..>330

67 a 107 c 83 g 71 t 2 others

BASE COUNT

ORIGIN

STS

Query Match

Best Local Similarity 100.0%; Score 12; DB 11; Length 330;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 1 gcctctgaggag 12

|||||

DB 80 GCCTCTGGGAG 91

Search completed: May 10, 2002, 16:15:54

Job time: 7024 sec

GenCore version 4.5
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OW nucleic - nucleic search, using sw model

Run on: May 10, 2002, 14:18:50 ; Search time 68.34 Seconds
(without alignments)
43.131 Million cell updates/sec

Title: US-09-761-116-1
perfect score: 12
Sequence: 1 gctctcgggag 12

Scoring table: IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/prodata/2/lna/5A_COMB.seq: *
2: /cgn2_6/prodata/2/lna/5B_COMB.seq: *
3: /cgn2_6/prodata/2/lna/6A_COMB.seq: *
4: /cgn2_6/prodata/2/lna/6B_COMB.seq: *
5: /cgn2_6/prodata/2/lna/PCTUS_COMB.seq: *
6: /cgn2_6/prodata/2/lna/Backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	100.0	12	4 US-09-243-335-1	Sequence 1, Appl
2	12	100.0	28	4 US-09-243-335-41	Sequence 41, Appl
3	12	100.0	28	4 US-09-243-335-46	Sequence 46, Appl
4	12	100.0	28	4 US-09-243-335-47	Sequence 47, Appl
5	12	100.0	28	4 US-09-243-335-48	Sequence 48, Appl
6	12	100.0	200	4 US-09-243-335-3	Sequence 3, Appl
7	12	100.0	1279	1 US-08-146-010A-4	Sequence 4, Appl
8	12	100.0	1279	1 US-08-674-168-9	Sequence 9, Appl
9	12	100.0	1363	5 US-08-776-088-21	Sequence 21, Appl
10	12	100.0	1363	5 PCT-US95-09145A-21	Sequence 21, Appl
11	12	100.0	1875	3 US-08-878-474-4	Sequence 4, Appl
12	12	100.0	1938	1 US-08-278-635B-1	Sequence 1, Appl
13	12	100.0	1938	3 US-08-464-258B-1	Sequence 1, Appl
14	12	100.0	1938	3 US-08-471-961-1	Sequence 1, Appl
15	12	100.0	2374	2 US-08-466-589-5	Sequence 5, Appl
16	12	100.0	2374	2 US-08-700-636-5	Sequence 5, Appl
17	12	100.0	2374	3 US-08-467-574-5	Sequence 5, Appl
18	12	100.0	2374	4 US-09-217-345-5	Sequence 5, Appl
19	12	100.0	2540	1 US-08-446-919A-1	Sequence 1, Appl
20	12	100.0	2577	2 US-08-209-521-25	Sequence 25, Appl
21	12	100.0	2655	4 US-08-456-200B-10	Sequence 10, Appl
22	12	100.0	4837	4 US-09-629-616-1	Sequence 1, Appl
23	12	100.0	5176	4 US-09-182-024A-1	Sequence 1, Appl
24	12	100.0	5434	2 US-08-841-349-1	Sequence 1, Appl
25	12	100.0	7032	2 US-08-149-097D-24	Sequence 24, Appl
26	12	100.0	7032	2 US-08-949-386-24	Sequence 24, Appl
27	12	100.0	7032	3 US-08-450-562-24	Sequence 24, Appl

c 28	12	100.0	7032	4 US-08-984-709A-24	Sequence 24, Appl
c 29	12	100.0	7089	3 US-08-949-386-25	Sequence 25, Appl
c 30	12	100.0	7089	3 US-08-450-562-25	Sequence 25, Appl
c 31	12	100.0	7089	4 US-08-984-709A-25	Sequence 25, Appl
c 32	12	100.0	8310	3 US-08-870-126-11	Sequence 11, Appl
c 33	12	100.0	14985	3 US-08-652-972A-6	Sequence 6, Appl
c 34	12	100.0	14985	3 PCT-US96-06231A-6	Sequence 6, Appl
c 35	11.6	96.7	130	3 US-08-577-081A-7	Sequence 7, Appl
c 36	11	91.7	60	4 US-08-406-030A-8	Sequence 8, Appl
c 37	11	91.7	60	4 US-08-406-030A-9	Sequence 8, Appl
c 38	11	91.7	342	1 US-08-235-83B-8	Sequence 8, Appl
c 39	11	91.7	342	2 US-08-465-473B-8	Sequence 8, Appl
c 40	11	91.7	371	4 US-08-961-810-36	Sequence 36, Appl
c 41	11	91.7	371	4 US-08-352-902D-36	Sequence 36, Appl
c 42	11	91.7	502	4 US-09-085-199B-39	Sequence 39, Appl
c 43	11	91.7	570	2 US-08-633-682-1	Sequence 1, Appl
c 44	11	91.7	570	3 US-08-936-772-1	Sequence 1, Appl
c 45	11	91.7	570	4 US-09-395-918-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-243-335-1
; Sequence 1, Application US/09243335A
; Patent No. 6197580
; GENERAL INFORMATION:
; APPLICANT: American Home Products Corp.
; APPLICANT: Susulic, Vedrana S.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF THE HUMAN
; TITLE OF INVENTION: B3-ADRENERGIC RECEPTOR GENE.
; FILE REFERENCE: 0630/05791
; CURRENT APPLICATION NUMBER: US/09/243,335A
; CURRENT FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-243-335-1

Query Match 100.0%; Score 12; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctctcgggag 12
|||||
DB 1 gctctcgggag 12

RESULT 2
US-09-243-335-41
; Sequence 41, Application US/09243335A
; Patent No. 6197580
; GENERAL INFORMATION:
; APPLICANT: American Home Products Corp.
; APPLICANT: Susulic, Vedrana S.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF THE HUMAN
; TITLE OF INVENTION: B3-ADRENERGIC RECEPTOR GENE
; FILE REFERENCE: 0630/05791
; CURRENT APPLICATION NUMBER: US/09/243,335A
; CURRENT FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 28

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide
US-09-243-335-41

Query Match 100.0%; Score 12; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggcctcgggag 12
|||||
Db 6 ggcctcgggag 17

RESULT 3
US-09-243-335-46
Sequence 46, Application US/09243335A
Patent No. 6197580
GENERAL INFORMATION:
APPLICANT: American Home Products Corp.
APPLICANT: Susulic, Vedrana S.
APPLICANT: Duzic, Edmir
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF THE HUMAN
FILE REFERENCE: 0630/0E791
CURRENT APPLICATION NUMBER: US/09/243.335A
CURRENT FILING DATE: 1999-02-01
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 46
LENGTH: 28
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide
US-09-243-335-46

Query Match 100.0%; Score 12; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggcctcgggag 12
|||||
Db 6 ggcctcgggag 17

RESULT 4
US-09-243-335-47
Sequence 47, Application US/09243335A
Patent No. 6197580
GENERAL INFORMATION:
APPLICANT: American Home Products Corp.
APPLICANT: Susulic, Vedrana S.
APPLICANT: Duzic, Edmir
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF THE HUMAN
FILE REFERENCE: 0630/0E791
CURRENT APPLICATION NUMBER: US/09/243.335A
CURRENT FILING DATE: 1999-02-01
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 47
LENGTH: 28
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide
US-09-243-335-47

Query Match 100.0%; Score 12; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggcctcgggag 12
|||||
Db 6 ggcctcgggag 17

RESULT 5
US-09-243-335-48
Sequence 48, Application US/09243335A
Patent No. 6197580
GENERAL INFORMATION:
APPLICANT: American Home Products Corp.
APPLICANT: Susulic, Vedrana S.
APPLICANT: Duzic, Edmir
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF THE HUMAN
FILE REFERENCE: 0630/0E791
CURRENT APPLICATION NUMBER: US/09/243.335A
CURRENT FILING DATE: 1999-02-01
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 48
LENGTH: 28
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide
US-09-243-335-48

Query Match 100.0%; Score 12; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggcctcgggag 12
|||||
Db 6 ggcctcgggag 17

RESULT 6
US-09-243-335-3
Sequence 3, Application US/09243335A
Patent No. 6197580
GENERAL INFORMATION:
APPLICANT: American Home Products Corp.
APPLICANT: Susulic, Vedrana S.
APPLICANT: Duzic, Edmir
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF THE HUMAN
FILE REFERENCE: 0630/0E791
CURRENT APPLICATION NUMBER: US/09/243.335A
CURRENT FILING DATE: 1999-02-01
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 200
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
US-09-243-335-3

Query Match 100.0%; Score 12; DB 4; Length 200;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggcctcgggag 12
|||||
Db 61 ggcctcgggag 72

RESULT 7
US-08-146-010A-4/C
; Sequence 4, Application US/08146010A
; Patent No. 5591577
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, MAKOTO
APPLICANT: MORIYA, MIKO
APPLICANT: MIMA, KIYOSHI
TITLE OF INVENTION: MOBILE GENETIC ELEMENT ORIGINATED FROM
TITLE OF INVENTION: BREVBACTERIUM STRAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,010A
FILING DATE: 12-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 52694/92
FILING DATE: 11-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-649-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1279 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
* ORGANISM: Brevibacterium lactofermentum
SPRAIN: AJ2256
FEATURE:
NAME/KEY: insertion_seq
LOCATION: 1..1279
US-08-146-010A-4

Query Match 100.0%; Score 12; DB 1; Length 1279;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gccctctggggag 12
|||||
DB 136 GCCCTCTGGGAG 125

RESULT 8
US-08-674-168-9/C
; Sequence 9, Application US/08674168
; Patent No. 5804414
GENERAL INFORMATION:
APPLICANT: MORIYA, MIKA
APPLICANT: MATSUI, HIROSHI
APPLICANT: YOKOZEKI, KENZO
APPLICANT: HIRANO, SEIKO

APPLICANT: HAYAKAWA, Atsushi
APPLICANT: IZUI, Masako
APPLICANT: SUGIMOTO, Masakazu
TITLE OF INVENTION: METHOD OF AMPLIFYING GENE USING
TITLE OF INVENTION: ARTIFICIAL TRANSPOSON
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/674,168
FILING DATE: 01-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-166541
FILING DATE: 30-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-810-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1279 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Brevibacterium lactofermentum
SPRAIN: AJ12036
FEATURE:
NAME/KEY: repeat_region
LOCATION: 1..14
FEATURE:
NAME/KEY: repeat_region
LOCATION: 1266..1279
US-08-674-168-9

Query Match 100.0%; Score 12; DB 1; Length 1279;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gccctctggggag 12
|||||
DB 136 GCCCTCTGGGAG 125

RESULT 9
US-08-776-088-21/C
; Sequence 21, Application US/08776088
; Patent No. 5773579
GENERAL INFORMATION:
APPLICANT: Torczynski, Richard M.
APPLICANT: Bollon, Arthur P.
TITLE OF INVENTION: Lung Cancer Marker
NUMBER OF SEQUENCES: 22

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: SIDLEY & AUSTIN
;; STREET: 1201 Elm Street, Suite 4500
;; CITY: Dallas
;; STATE: TX
;; COUNTRY: US
;; ZIP: 75270-2197
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: Patent Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/776,088
;; FILING DATE: 19-JUL-95
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Eugenia S. Hansen
;; REGISTRATION NUMBER: 31,966
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 214-981-3300
;; TELEFAX: 214-981-3400
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1363 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-08-776-088-21

Query Match 100.0%; Score 12; DB 1; Length 1363;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggcctcggggag 12
|||||
DB 183 gccctctggggag 172

RESULT 10
PCT-US95-09145A-21/C
; Sequence 21, Application PC/TUS9509145A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Lung Cancer Marker
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
; STREET: 1201 Elm Street, Suite 4500
; CITY: Dallas
; STATE: TX
; COUNTRY: US
; ZIP: 75270-2197
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09145A
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: John A. Harre
; REGISTRATION NUMBER: 37,345
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 214-939-4500
; TELEFAX: 214-939-4600
; INFORMATION FOR SEQ ID NO: 21:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1363 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; PCT-US95-09145A-21

Query Match 100.0%; Score 12; DB 5; Length 1363;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggcctcggggag 12
|||||
DB 183 gccctctggggag 172

RESULT 11
US-08-878-474-4/C
; Sequence 4, Application US/08878474
; Patent No. 6133232
; GENERAL INFORMATION:
; APPLICANT: De Robertis, Edward M.
; APPLICANT: Boumeester, Lewis
; TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
; TITLE OF INVENTION: Factors
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/878,474
; FILING DATE: 18-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US 60/020,150
; FILING DATE: 20-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Siebert, J. Suzanne
; REGISTRATION NUMBER: 28,758
; REFERENCE/DOCKET NUMBER: 3100.002US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/248-5500
; TELEFAX: 415/362-5418
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1875 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-878-474-4

Query Match 100.0%; Score 12; DB 3; Length 1875;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggcctcggggag 12
|||||
DB 769 gccctctggggag 758

RESULT 12
US-08-278-635B-1
Sequence 1, Application US/08278635B
Patent No. 5683912
GENERAL INFORMATION:
APPLICANT: ELGOYHEN, ANA BELEN
APPLICANT: JOHNSON, DAVID S.
APPLICANT: BOULTER, JAMES R.
APPLICANT: HEINEMANN, STEPHEN F.
TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAY CARY WARE & FREIDENRICH
STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,635B
FILING DATE: 21-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9771
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1938 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: ALPHA 9
FEATURE:
NAME/KEY: CDS
LOCATION: 89..1525
US-08-278-635B-1

Query Match 100.0%; Score 12; DB 1; Length 1938;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gccctcgggag 12
|||||
DB 878 GCCTCTGGGAG 889

RESULT 13
US-08-464-258B-1
Sequence 1, Application US/08464258B
Patent No. 6013766
GENERAL INFORMATION:
APPLICANT: ELGOYHEN, ANA BELEN
APPLICANT: JOHNSON, DAVID S.
APPLICANT: BOULTER, JAMES R.
APPLICANT: HEINEMANN, STEPHEN F.
TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAY CARY WARE & FREIDENRICH
STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAY CARY WARE & FREIDENRICH LLP
STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,258B
FILING DATE: 06/05/95
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/278,635
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9989
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1938 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: ALPHA 9
FEATURE:
NAME/KEY: CDS
LOCATION: 89..1525
US-08-464-258B-1

Query Match 100.0%; Score 12; DB 3; Length 1938;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gccctcgggag 12
|||||
DB 878 GCCTCTGGGAG 889

RESULT 14
US-08-471-961-1
Sequence 1, Application US/08471961
Patent No. 6100046
GENERAL INFORMATION:
APPLICANT: ELGOYHEN, ANA BELEN
APPLICANT: JOHNSON, DAVID S.
APPLICANT: BOULTER, JAMES R.
APPLICANT: HEINEMANN, STEPHEN F.
TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAY CARY WARE & FREIDENRICH
STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471.961
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,635
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9771
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1938 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: ALPHA 9
FEATURE:
NAME/KEY: CDS
LOCATION: 89..1525
US-08-471-961-1

Query Match 100.0%; Score 12; DB 3; Length 1938;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcctctggggag 12
|||||
DB 878 GCCTCTGGGGAG 889

RESULT 15
US-08-466-589-5
Sequence 5, Application US/08466589
Patent No. 5837489
GENERAL INFORMATION:
APPLICANT: Elliot, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,589
FILING DATE: June 5, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: March 8, 1993

```

```

ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9950
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2374 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 184..2067
US-08-466-589-5

Query Match 100.0%; Score 12; DB 2; Length 2374;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcctctggggag 12
|||||
DB 2237 GCCTCTGGGGAG 2248

Search completed: May 10, 2002, 15:39:25
Job time: 4835 sec

```


PT New isolated nucleic acid useful for screening assays to identify compounds capable of regulating beta3-AR (adrenergic receptor)

PT expression, is composed of three regulatory segments -
XX
PS Claim 2: Page 57; 88pp; English.
XX
CC The present sequence represent the core nucleotide sequence from the
CC B segment of the human beta-3-adrenergic receptor (beta-3-AR) regulatory
CC region. The core nucleotide sequence binds to a B-segment-binding
CC trans-activating factor. Recombinant vectors under control of the
CC transcription regulation region comprising nucleotide sequences
CC containing the core nucleotide sequence from the B segment of the human
CC beta-3-AR regulatory region provide a substrate for high throughput
CC assays, particularly reporter gene assays to identify compounds capable
CC of increasing or decreasing the level of expression of beta-3-AR. The
CC nucleotide sequences can be used for regulating gene expression and for
CC drug screening. It is envisaged that beta-3-AR stimulation may have
CC beneficial effects in the treatment of obesity and type II diabetes.
XX
SQ Sequence 12 BP; 1 A; 3 C; 6 G; 2 T; 0 other;

Query Match 100.0%; Score 12; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggcctcggggag 12
|||||
DB 1 ggcctcggggag 12

RESULT 2
AAA87942
ID AAA87942 standard; DNA; 28 BP.
AC AAA87942;
XX
DT 07-DEC-2000 (first entry)
XX
DE Beta-3-AR segment B mutational analysis oligonucleotide SEQ ID NO:41.
XX
KW Human; beta-3-adrenergic receptor; beta-3-AR; transcription; promoter;
KW regulation; identification; trans-activating factor; drug screening;
KW gene expression regulation; obesity; type II diabetes; mutation; ss.
XX
OS Homo sapiens.
XX
PN WO200044901-A1.
XX
PD 03-AUG-2000.
XX
XX 01-FEB-2000; 2000WO-US02632.
XX
XX 01-FEB-1999; 99US-0243335.
XX
PA (AMHP) AMERICAN HOME PROD CORP.
XX
PI Susulic VS, Duzic E;
XX
DR WPI; 2000-482973/42.
XX
PT New isolated nucleic acid useful for screening assays to identify
PT compounds capable of regulating beta3-AR (adrenergic receptor)
PT expression, is composed of three regulatory segments -
XX
PS Example 1; Fig 7; 88pp; English.
XX
CC The present invention describes a core nucleotide sequence from the
CC B segment of the human beta-3-adrenergic receptor (beta-3-AR) regulatory
CC region. The core nucleotide sequence binds to a B-segment-binding
CC trans-activating factor. Recombinant vectors under control of the
CC transcription regulation region comprising nucleotide sequences
CC containing the core nucleotide sequence from the B segment of the human
CC beta-3-AR regulatory region provide a substrate for high throughput
CC assays, particularly reporter gene assays to identify compounds capable
CC of increasing or decreasing the level of expression of beta-3-AR. The
CC nucleotide sequences can be used for regulating gene expression and for
CC drug screening. It is envisaged that beta-3-AR stimulation may have
CC beneficial effects in the treatment of obesity and type II diabetes.
CC The present sequence represents a human beta-3-AR segment B mutational
CC analysis oligonucleotide, which is used in the exemplification of the
CC present invention.
XX
SQ Sequence 12 BP; 1 A; 3 C; 6 G; 2 T; 0 other;

CC of increasing or decreasing the level of expression of beta-3-AR. The
CC nucleotide sequences can be used for regulating gene expression and for
CC drug screening. It is envisaged that beta-3-AR stimulation may have
CC beneficial effects in the treatment of obesity and type II diabetes.
CC The present sequence represents a human beta-3-AR segment B mutational
CC analysis oligonucleotide, which is used in the exemplification of the
CC present invention.
XX
SQ Sequence 28 BP; 4 A; 10 C; 8 G; 6 T; 0 other;

Query Match 100.0%; Score 12; DB 21; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggcctcggggag 12
|||||
DB 6 ggcctcggggag 17

RESULT 3
AAA87947
ID AAA87947 standard; DNA; 28 BP.
AC AAA87947;
XX
DT 07-DEC-2000 (first entry)
XX
DE Beta-3-AR segment B mutational analysis oligonucleotide SEQ ID NO:46.
XX
KW Human; beta-3-adrenergic receptor; beta-3-AR; transcription; promoter;
KW regulation; identification; trans-activating factor; drug screening;
KW gene expression regulation; obesity; type II diabetes; mutation; ss.
XX
OS Homo sapiens.
XX
PN WO200044901-A1.
XX
PD 03-AUG-2000.
XX
XX 01-FEB-2000; 2000WO-US02632.
XX
XX 01-FEB-1999; 99US-0243335.
XX
PA (AMHP) AMERICAN HOME PROD CORP.
XX
PI Susulic VS, Duzic E;
XX
DR WPI; 2000-482973/42.
XX
PT New isolated nucleic acid useful for screening assays to identify
PT compounds capable of regulating beta3-AR (adrenergic receptor)
PT expression, is composed of three regulatory segments -
XX
PS Example 1; Fig 7; 88pp; English.
XX
CC The present invention describes a core nucleotide sequence from the
CC B segment of the human beta-3-adrenergic receptor (beta-3-AR) regulatory
CC region. The core nucleotide sequence binds to a B-segment-binding
CC trans-activating factor. Recombinant vectors under control of the
CC transcription regulation region comprising nucleotide sequences
CC containing the core nucleotide sequence from the B segment of the human
CC beta-3-AR regulatory region provide a substrate for high throughput
CC assays, particularly reporter gene assays to identify compounds capable
CC of increasing or decreasing the level of expression of beta-3-AR. The
CC nucleotide sequences can be used for regulating gene expression and for
CC drug screening. It is envisaged that beta-3-AR stimulation may have
CC beneficial effects in the treatment of obesity and type II diabetes.
CC The present sequence represents a human beta-3-AR segment B mutational
CC analysis oligonucleotide, which is used in the exemplification of the
CC present invention.
XX
SQ Sequence 28 BP; 3 A; 10 C; 8 G; 7 T; 0 other;


```

XX Human foetal liver single exon nucleic acid probe #24561.
DE
XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
KW
XX Homo sapiens.
OS
XX WO200157277-A2.
PN
XX
XX
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US000669.
PE
XX
XX 04-FEB-2000; 2000US-0180312.
PR
XX 26-MAY-2000; 2000US-0207456.
PR
XX 30-JUN-2000; 2000US-0608408.
PR
XX 03-AUG-2000; 2000US-0632366.
PR
XX 21-SEP-2000; 2000US-0234687.
PR
XX 27-SEP-2000; 2000US-0236359.
PR
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human fetal liver.
XX
XX Claim 4; SEQ ID NO 24561; 639pp + sequence listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for
XX measuring human gene expression in a sample derived from human foetal
XX liver. The single exon nucleic acid probes may be used for predicting,
XX measuring and displaying gene expression in samples derived from human
XX fetal liver. The present sequence is a single exon nucleic acid
XX probe of the invention.
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 113 BP; 7 A; 44 C; 29 G; 33 T; 0 other;
SQ

```

```

Query Match          100.0%; Score 12; DB 22; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
          1 gccctctggggag 12
          |||
          94 gccctctggggag 105

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```

RESULT 7
ABA40796
ID ABA40796 standard; DNA; 113 BP.
XX
XX ABA40796;
AC
XX
XX 23-JAN-2002 (first entry)
DT
XX
XX Probe #19262 for gene expression analysis in human heart cell sample.
DE
XX
XX Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
XX Homo sapiens.
OS
XX WO200157274-A2.
PN
XX
XX 09-AUG-2001.
PD

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XX
XX 30-JAN-2001; 2001WO-US00066.
PF
XX
XX 04-FEB-2000; 2000US-0180312.
PR
XX 26-MAY-2000; 2000US-0207456.
PR
XX 30-JUN-2000; 2000US-0608408.
PR
XX 03-AUG-2000; 2000US-0632366.
PR
XX 21-SEP-2000; 2000US-0234687.
PR
XX 27-SEP-2000; 2000US-0236359.
PR
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488899/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts.
XX
XX Claim 4; SEQ ID NO 19262; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart. The
XX present sequence is one such probe. The probes may be used for
XX predicting, measuring and displaying gene expression in samples derived
XX from the human heart via microarrays. By measuring gene expression, the
XX probes are useful for predicting, diagnosing, grading, staging,
XX monitoring and prognosticating diseases of the human heart and vascular system
XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX congenital heart disease.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 113 BP; 7 A; 44 C; 29 G; 33 T; 0 other;
SQ

```

```

Query Match          100.0%; Score 12; DB 22; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
          1 gccctctggggag 12
          |||
          94 gccctctggggag 105

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```

RESULT 8
AAK24907
ID AAK24907 standard; DNA; 113 BP.
XX
XX AAK24907;
AC
XX
XX 05-NOV-2001 (first entry)
DT
XX
XX Human brain expressed single exon probe SEQ ID NO: 24898.
DE
XX
XX Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
XX
XX Homo sapiens.
OS
XX WO200157275-A2.
PN
XX
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US000669.
PE
XX
XX 04-FEB-2000; 2000US-0180312.
PR
XX 26-MAY-2000; 2000US-0207456.
PR
XX 30-JUN-2000; 2000US-0608408.
PR
XX 03-AUG-2000; 2000US-0632366.

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XX 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.

XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI: 2001-483446/52.
XX

PS Example 4; SEQ ID NO: 24898; 650bp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention.
CO

SQ Sequence 113 BP; 7 A; 44 C; 29 G; 33 T; 0 other;

OY 1 gcctctggaggag 12
|||
Db 94 gccctctggaggag 105

RESULT 9
AAK50902
ID AAK50902 standard; DNA: 113 BP.
XX
AC AAK50902;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 25459.
XX
KM Human; bone marrow expressed exon; gene expression analysis; probe;
KM microarray; cancer; leukemia; lymphoma; myeloma; ss.
XX
OS Homo sapiens.
XX
PM WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00668.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-063366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI: 2001-488900/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human bone marrow -

```

XX Example 4; SEQ ID NO: 25459; 658bp + Sequence Listing; English.
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention.
XX
SQ Sequence 113 BP; 7 A; 44 C; 29 G; 33 T; 0 other;

Query Match          100.0%; Score 12; DB 22; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gccctctggggag 12
   |||
Db 94 gccctctggggag 105

RESULT 10
AA127940
ID AA127940 standard; DNA; 113 BP.
XX
AC AA127940;
XX
DT 12-OCT-2001 (first entry)
DE Probe #17873 for gene expression analysis in human cervical cell sample.
XX
KM Probe; human; microarray; gene expression; cervical epithelial cell;
KM cervical cancer; ss.
XX
OS Homo sapiens.
XX
WO200157278-A2.
XX
PN 09-AUG-2001.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00670.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAR-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488901/53.
XX
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX
XX
Claim 25; SEQ ID NO 17873; 487bp; English.
XX
XX
The present invention relates to human single exon nucleic acid probes
(SNMP). The present sequence is one such probe. The SNMPs are derived
from human HeLa cells. The SNMPs can be used to produce a single exon
microarray, which can be used for measuring human gene expression in a
sample derived from human cervical epithelial cells. By measuring gene
expression, the probes are therefore useful in grading and/or staging
of diseases of the cervix, notably cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
Sequence 113 BP; 7 A; 44 C; 29 G; 33 T; 0 other;

```

Query Match 100.0%; Score 12; DB 22; Length 113;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcctctggggag 12
 |||||
 DB 94 gcctctggggag 105

RESULT 11

AAA87904
 ID AAA87904 standard; DNA; 200 BP.

AC AAA87904;

DT 07-DEC-2000 (first entry)

DE Human beta-3-adrenergic receptor 5' flanking region SEQ ID NO:3.

XX Human; beta-3-adrenergic receptor; beta-3-AR; transcription; promoter;
 regulation; identification; trans-activating factor; drug screening;
 gene expression regulation; obesity; type II diabetes; ds.

OS Homo sapiens.

MO200044901-A1.

PD 03-AUG-2000.

PF 01-FEB-2000; 2000MO-US02632.

PR 01-FEB-1999; 99US-0243335.

PA (AMHP) AMERICAN HOME PROD CORP.

PI Susulic VS, Duzic E;

WI; 2000-482973/42.

PT New isolated nucleic acid useful for screening assays to identify
 compounds capable of regulating beta3-AR (adrenergic receptor)
 expression, is composed of three regulatory segments -

Claim 10; Fig 6A; 88pp; English.

CC The present invention describes a core nucleotide sequence from the
 B segment of the human beta-3-adrenergic receptor (beta-3-AR) regulatory
 region. The core nucleotide sequence binds to a B-segment-binding
 trans-activating factor. Recombinant vectors under control of the
 transcription regulation region comprising nucleotide sequences
 containing the core nucleotide sequence from the B segment of the human
 beta-3-AR regulatory region provide a substrate for high throughput
 assays, particularly reporter gene assays to identify compounds capable
 of increasing or decreasing the level of expression of beta-3-AR. The
 nucleotide sequences can be used for regulating gene expression and for
 drug screening. It is envisaged that beta-3-AR stimulation may have
 beneficial effects in the treatment of obesity and type II diabetes.
 CC The present sequence represents the human beta-3-adrenergic receptor 5'
 flanking region, which is used in the exemplification of the present
 CC invention.

XX Sequence 200 BP; 25 A; 70 C; 37 G; 68 T; 0 other;

Query Match 100.0%; Score 12; DB 21; Length 200;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcctctggggag 12
 |||||
 DB 61 gcctctggggag 72

RESULT 12

AAC15250/C
 ID AAC15250 standard; cDNA; 227 BP.

AC AAC15250;

DT 06-OCT-2000 (first entry)

DE Human secreted protein 5' EST, SEQ ID NO: 19325.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 gene therapy; chromosome mapping; ss.

OS Homo sapiens.

PN EP1033401-A2.

PD 06-SEP-2000.

PF 21-FEB-2000; 2000EP-0200610.

PR 26-FEB-1999; 99US-0122487.

PA (GEST) GENSET.

PI Dumas Milne Edwards J, Duclert A, Giordano J;

WI; 2000-500381/45.

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 diagnostic, forensic, gene therapy and chromosome mapping procedures -
 Claim 1; SEQ ID 19325; 71pp + CD-ROM; English.

CC The present sequence is one of a large number of 5' ESTs derived from
 mRNAs encoding secreted proteins. No ORF has yet been conclusively
 identified within the present sequence. The 5' ESTs were prepared from
 total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 sequences usually correspond mainly to the 3' untranslated region (UTR)
 of the mRNA because they are often obtained from oligo-dT primed cDNA
 libraries. Such ESTs are not well suited for isolating cDNA sequences
 derived from the 5' ends of mRNAs and even in those cases where longer
 cDNA sequences have been obtained, the full 5' UTR is rarely included.
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
 used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
 in diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors.

XX Sequence 227 BP; 50 A; 53 C; 67 G; 53 T; 4 other;

Query Match 100.0%; Score 12; DB 21; Length 227;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcctctggggag 12
 |||||
 DB 169 GCCTCTGGGGAG 158

RESULT 13

AAS30782
 ID AAS30782 standard; cDNA; 234 BP.

AC AAS30782;

DT 04-DEC-2001 (first entry)

DE Human cDNA encoding G protein-coupled receptor ngPCR-83.

XX Human: G protein-coupled receptor: ngPCR-x: ss: antiviral: analgesic;
KM cyclostatic; caritant; antidiabetic; anorectic; hypotensive; hypertensive;
KM antiparkinsonian; nootropic; neuroprotective; antidepressant;
KM viral infection: HIV-1; human immunodeficiency virus; HIV-2; pain;
KM cancer; metabolic disease; cardiovascular disease; type 2 diabetes;
KM obesity; anorexia; hypotension; hypertension; myocardial infarction;
KM atherosclerosis; Parkinson's disease; psychosis; neurological disorder;
KM schizophrenia; migraine; major depression; anxiety; mental disorder;
KM manic depression; dyskinesia; Huntington's disease; Tourette's Syndrome.
XX
OS Homo sapiens.
XX
PN WC20016750-A2.
XX
PD 13-SEP-2001.
XX
PF 08-MAR-2001; 2001WO-US07322.
XX
PR 08-MAR-2000; 2000US-0187581.
PR 08-MAR-2000; 2000US-0187582.
PR 08-MAR-2000; 2000US-0187714.
PR 08-MAR-2000; 2000US-0187715.
PR 08-MAR-2000; 2000US-0187825.
PR 08-MAR-2000; 2000US-0187828.
PR 08-MAR-2000; 2000US-0187829.
PR 08-MAR-2000; 2000US-0187830.
PR 08-MAR-2000; 2000US-0187833.
PR 08-MAR-2000; 2000US-0187874.
PR 08-MAR-2000; 2000US-0187930.
PR 08-MAR-2000; 2000US-0188049.
PR 08-MAR-2000; 2000US-0189294.
PR 08-MAR-2000; 2000US-0189299.
PR 08-MAR-2000; 2000US-0189298.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Vogell G, Wood LS;
XX
DR WPI: 2001-536778/59.
XX
DR P-PSDB; AAU19213.
XX
PT Isolated nucleic acid molecules encoding G protein-coupled receptors
PT termed ngPCR-x, useful in the treatment and diagnosis of viral
PT infections, cancers and mental disorders (e.g. Parkinson's disease and
PT schizophrenia) -
XX
PS
PS Claim 4; Page 201; 336pp; English.
XX
CC The invention relates to novel isolated nucleic acid molecules encoding
CC G protein-coupled receptors termed ngPCR-x. ngPCR-x polynucleotides,
CC polypeptides, and modulators may be used in the treatment of diseases and
CC conditions such as infections, such as viral infections caused by HIV-1
CC (human immunodeficiency virus) or HIV-2, pain, cancers, metabolic and
CC cardiovascular diseases and disorders (e.g., type 2 diabetes, obesity,
CC anorexia, hypotension, hypertension, myocardial infarction,
CC atherosclerosis), Parkinson's disease, and psychotic and
CC neurological disorders, including schizophrenia, migraine, major
CC depression, anxiety, mental disorder, manic depression, and
CC dyskinesias, such as Huntington's disease or Tourette's Syndrome
CC and many other diseases and syndromes listed in the specification.
CC ngPCR-x polynucleotides and polypeptides, as well as ngPCR-x
CC modulators, may also be used in diagnostic assays for such diseases or
CC conditions. The present sequence encodes a G protein-coupled
CC receptor of the invention.
XX
SQ Sequence 234 BP; 56 A; 64 C; 65 G; 49 T; 0 other;

Query Match 100.0%; Score 12; DB 22; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcctctggggag 12
Db 100 gcctctggggag 111
RESULT 14
AAC48449
ID AAC48449 standard; DNA; 294 BP.
XX
AC AAC48449;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 57523.
XX
KM Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway;
KM metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 14-MAY-1999; 99US-0134376.
PR 18-MAY-1999; 99US-0134941.
PR 19-MAY-1999; 99US-0135124.
PR 20-MAY-1999; 99US-0135353.
PR 21-MAY-1999; 99US-0135629.
PR 24-MAY-1999; 99US-0136021.
PR 25-MAY-1999; 99US-0136392.
PR 27-MAY-1999; 99US-0136782.
PR 28-MAY-1999; 99US-0137222.
PR 01-JUN-1999; 99US-0137526.
PR 03-JUN-1999; 99US-0137502.
PR 04-JUN-1999; 99US-0137724.
PR 07-JUN-1999; 99US-0138094.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.

PR 18-JUN-1999; 99US-0139454.
 PR 18-JUN-1999; 99US-0139455.
 PR 18-JUN-1999; 99US-0139456.
 PR 18-JUN-1999; 99US-0139457.
 PR 18-JUN-1999; 99US-0139458.
 PR 18-JUN-1999; 99US-0139459.
 PR 18-JUN-1999; 99US-0139460.
 PR 18-JUN-1999; 99US-0139461.
 PR 18-JUN-1999; 99US-0139462.
 PR 18-JUN-1999; 99US-0139463.
 PR 18-JUN-1999; 99US-0139750.
 PR 18-JUN-1999; 99US-0139763.
 PR 22-JUN-1999; 99US-0139817.
 PR 23-JUN-1999; 99US-0140353.
 PR 23-JUN-1999; 99US-0140354.
 PR 24-JUN-1999; 99US-0140695.
 PR 28-JUN-1999; 99US-0140823.
 PR 29-JUN-1999; 99US-0140991.
 PR 30-JUN-1999; 99US-0141287.
 PR 01-JUL-1999; 99US-0141842.
 PR 02-JUL-1999; 99US-0142154.
 PR 06-JUL-1999; 99US-0142055.
 PR 08-JUL-1999; 99US-0142290.
 PR 09-JUL-1999; 99US-0142803.
 PR 12-JUL-1999; 99US-0142920.
 PR 13-JUL-1999; 99US-0143542.
 PR 14-JUL-1999; 99US-0143624.
 PR 15-JUL-1999; 99US-0144005.
 PR 16-JUL-1999; 99US-0144085.
 PR 16-JUL-1999; 99US-0144086.
 PR 19-JUL-1999; 99US-0144325.
 PR 19-JUL-1999; 99US-0144331.
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ID ABA51365 standard; DNA; 305 BP.
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 DT 01-FEB-2002 (first entry)
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 DE Human breast cell single exon nucleic acid probe #10060.
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 KW Human; microarray; single exon probe; gene expression; breast;
 XX disease; cancer; ss.
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 PN W0200157271-A2.
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 PF 30-JAN-2001; 2001WO-US00662.
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 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SC, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI: 2001-496933/54.
 XX
 PA New spatially-addressable set of single exon nucleic acid probes,
 PT useful for measuring gene expression in sample derived from human
 PT breast, comprises number of single exon nucleic acid probes
 XX
 PS Claim 4; SEQ ID NO 10060; 327bp + sequence listing; English.
 XX
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and BR 474 cells. The method involves contacting
 CC the probes with a collection of detectably labelled nucleic acids
 CC derived from mRNA of human breast, and then measuring the label
 CC bound to each probe of the microarray. The probes are useful for
 CC verifying the expression of regions of genomic DNA predicted to
 CC encode proteins. They are useful for gene discovery, and for
 CC determining predisposition and/or prognosing breast disease. Gene
 CC expression analysis is useful for assessing the toxicity of chemical
 CC agents on cells. The microarray of this invention presents a far greater
 CC diversity of probes for measuring gene expression, with far less bias
 CC than expressed sequence tag microarrays. The method is suitable for
 CC rapid production of functional information from genomic sequence. The
 CC present sequence is a single exon nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIP0 at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 305 BP; 90 A; 67 C; 110 G; 38 T; 0 other;

Query Match 100.0%; Score 12; DB 22; Length 305;
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 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Mon May 13 08:57:59 2002

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